



Naoki Konno

Postdoctoral Scholar, Genetics

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BIO

Naoki has extensive training in evolutionary biology and bioinformatics, and he thrives in interdisciplinary environments bridging computation and developmental biology. After earning his BSc. and MSc. in Systems Biology and Bioinformatics at the University of Tokyo, Naoki pursued a PhD in Evolutionary Biology under the supervision by Prof. Chikara Furusawa. He has developed computational frameworks to reconstruct and predict evolutionary processes, including large-scale phylogenetic inference for both evolution and cell lineage tracing (FRACTAL) and predictive models of microbial genome evolution (Evodictor). His work revealed generalizable rules of genome evolution and was recognized with multiple awards, including the JSPS Ikushi Prize.

Currently, Naoki is a Postdoctoral Scholar in the lab of Prof. Xiaojie Qiu at Stanford University School of Medicine. In his postdoctoral research, he investigates the evolutionary constraints of vertebrate development with a focus on the heart as a model system. By integrating single-cell and spatial transcriptomics with predictive modeling and CRISPR-based perturbations, he seeks to uncover how evolutionary principles shape developmental trajectories and contribute to congenital heart defects. Ultimately, Naoki aims to establish a broad research program in evolution-aware medicine, connecting evolutionary theory with biomedical challenges.

HONORS AND AWARDS

- AHA Postdoctoral Fellowship, American Heart Association (2026)
- Inoue Research Award for Young Scientists, Inoue Foundation for Science (2026)
- Young Investigators Award, Society of Genome Microbiology, Japan (2026)
- JSPS Ikushi Prize, Japan Society for the Promotion of Science (2024)
- University of Tokyo President's Award, The University of Tokyo (2022)

STANFORD ADVISORS

- Xiaojie Qiu, Postdoctoral Faculty Sponsor

LINKS

- Personal website: <https://sites.google.com/view/naoki-konno/>
- Google Scholar: <https://scholar.google.co.jp/citations?user=TY6BaUEAAAAJ&hl=ja>

Publications

PUBLICATIONS

- **Fructophilic lactic acid bacteria as a window into multi-scale convergent evolution.** *Current opinion in microbiology*
Konno, N., Maeno, S., Endo, A.
2026; 93: 102815
- **Cooperation and the evolution of bacterial niche breadth.** *Proceedings of the National Academy of Sciences of the United States of America*
Hao, C., Konno, N., Ito, M., Belcher, L. J., Iwasaki, W., West, S. A.
2026; 123 (10): e2520645123
- **Host range and antibiotic resistance dissemination are shaped by distinct survival strategies of conjugative plasmids.** *Nucleic acids research*
Ono, R., Konno, N., Nishimura, Y., Furusawa, C.
2026; 54 (2)
- **Widespread promiscuous alkaline phosphatases underscore ancient microbial phosphite utilization.** *Proceedings of the National Academy of Sciences of the United States of America*
Sakuma, M., Konno, N., Gholipour, S., Chen, J. Z., Tokuriki, N.
2025; 122 (49): e2513042122
- **Repeatability of protein structural evolution following convergent gene fusions.** *Nature communications*
Konno, N., Miyake, K., Nishino, S., Omae, K., Yanagisawa, H., Tsuru, S., Nishimura, Y., Kikkawa, M., Furusawa, C., Iwasaki, W.
2025; 16 (1): 8278
- **Meeting Report: The First Evo-Devo Young Researchers Meeting.** *Development, growth & differentiation*
Uchida, Y., Ishida, T., Ono, S., Kuroda, S., Kobayashi, A., Konno, N., Tanaka, Y., Nishizawa, T., Yoshida, J., Yoshimoto, K. I., Yoneda, M.
2025; 67 (6): 331-335
- **Evolutionary paths toward multi-level convergence of lactic acid bacteria in fructose-rich environments.** *Communications biology*
Konno, N., Maeno, S., Tanizawa, Y., Arita, M., Endo, A., Iwasaki, W.
2024; 7 (1): 902
- **Machine learning enables prediction of metabolic system evolution in bacteria.** *Science advances*
Konno, N., Iwasaki, W.
2023; 9 (2): eadc9130
- **Molecular recorders to track cellular events.** *Science (New York, N.Y.)*
Masuyama, N., Konno, N., Yachie, N.
2022; 377 (6605): 469-470
- **Deep distributed computing to reconstruct extremely large lineage trees.** *Nature biotechnology*
Konno, N., Kijima, Y., Watano, K., Ishiguro, S., Ono, K., Tanaka, M., Mori, H., Masuyama, N., Pratt, D., Ideker, T., Iwasaki, W., Yachie, N.
2022; 40 (4): 566-575